1

SEQUENCE LISTING

<110> GIORGI, DOMINIQUE
      SAFFIN, JEAN-MICHEL
      ROUQUIER, SYLVIE

<120> NOVEL CENTROSOME-ASSOCIATED PROTEIN AND APPICATIONS
      THEREOF

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<140> 10/540,493
<141> 2005-06-24

<150> PCT/FR03/003895
<151> 2003-12-24

<150> FR 02 16648
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<170> PatentIn Ver. 3.3

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Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser Phe Ser Glu Ser Gln
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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens

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<213> Homo sapiens
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<213> Homo sapiens
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<213> Homo sapiens
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<211> 71
<212> DNA
<213> Homo sapiens
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<212> DNA
<213> Homo sapiens
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<213> Homo sapiens

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<223> Description of Artificial Sequence: Synthetic
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<213> Artificial Sequence

<220>
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<220>
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      primer

<400> 33
atcatttgag gcctggaagg c                                              21
```


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<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 34
aaacactttt gcgaacacag ttc                                            23
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```
<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 35
acaacgaata acagagtgtc c                                          21


<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 36
actcctgata aacagctgcc                                            20


<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 37
gccaccatgt ctgatgaagt ttttagcac                                  29


<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 38
gaaacacttt tgcgaacaca gttc                                       24


<210> 39
<211> 26
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 39
taatgtctga tgaagttttt agcacc   26

<210> 40
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 40
tcaaaacact tttgcgaaca cagttc   26

<210> 41
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 41
aatgtctgat gaagtttta gcacc   25

<210> 42
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 42
tcagcttgcc gtaggtggc   19

<210> 43
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 43
atggtcctgc tggagttcg   19

```
<210> 44
<211> 391
<212> DNA
<213> Mus musculus

<400> 44
aaagaagtga agacagaaac acgaagaata aaaagacaac gaataacaga gtgtccagtg 60
cctctggcag gctgatgacc tctgagtttt taaagagatc cggtcccaca aaaagaagtc 120
catctgcagc tacctcctca cactatttag ggagtttgaa agtcttggac cagaagcaac 180
cacggaagca gagcctagag ccagacaagg ctgatcacat aagggcagct gtttatcagg 240
agtggttaga aaagaaaaat gtgtatttac atgaaatgca cagaataaaa agaattgaaa 300
gcgaaaactt gaggatccaa aatgaacaga aaaaagctgc taagagagag gaagccctgg 360
catcatttga ggcctggaag gcaatgaaag a                            391


<210> 45
<211> 2767
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (204)..(2147)

<400> 45
gttgggtacc caagagacca ggcggttgga agtcacttcc tcccggggac gctgttgcct 60

agcaaccgcc ttctgcctcc atcttttgcc ccgcctccag gttattccaa tacctggttt 120

cccagaccgc gaggcccggg ccggggcga cacctgtgct agagcatagc cgctgggttc 180

tcagcagaga aaaaggacac acc atg tcc gat gaa atc ttc agc aca act ttg 233
                         Met Ser Asp Glu Ile Phe Ser Thr Thr Leu
                          1               5                  10


gcg tac acc aag agt cca aag gct acc aag aga act tcc ttt cag gat    281
Ala Tyr Thr Lys Ser Pro Lys Ala Thr Lys Arg Thr Ser Phe Gln Asp
              15                  20                  25


gag ctg atc aga gcc att aca gcc cgg tca gcc agg cag aga agt tcc    329
Glu Leu Ile Arg Ala Ile Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser
             30                  35                  40


gaa tac tcc gat gac ttt gac agt gac gag att gtt tct tta ggt gaa    377
Glu Tyr Ser Asp Asp Phe Asp Ser Asp Glu Ile Val Ser Leu Gly Glu
         45                  50                  55


ttt tca gat acc tcg aca gat gaa agt cta gtt aga aaa aag atg aat    425
Phe Ser Asp Thr Ser Thr Asp Glu Ser Leu Val Arg Lys Lys Met Asn
     60                  65                  70


gat ttt cat ata tcc gac gat gag gaa aaa aat tct cca aga ctg tct    473
Asp Phe His Ile Ser Asp Asp Glu Glu Lys Asn Ser Pro Arg Leu Ser
 75                  80                  85                  90
```

```
ttt ttg aaa acc aag aaa gta aac agg gca ata tcc aac gat gct ctg   521
Phe Leu Lys Thr Lys Lys Val Asn Arg Ala Ile Ser Asn Asp Ala Leu
             95              100             105

gac tcc agc act ccg ggc agc gaa ggc tcg tca ccg gat gct caa gaa   569
Asp Ser Ser Thr Pro Gly Ser Glu Gly Ser Ser Pro Asp Ala Gln Glu
             110             115             120

gat gtg act gga gat tcc ctc ccc aaa tct caa aat gat gat cga gaa   617
Asp Val Thr Gly Asp Ser Leu Pro Lys Ser Gln Asn Asp Asp Arg Glu
             125             130             135

gtc ggc aga gag atc atc aca gtg aag cct aca ccc agg atg cac ccc   665
Val Gly Arg Glu Ile Ile Thr Val Lys Pro Thr Pro Arg Met His Pro
             140             145             150

gtc aaa aga agc acg tcc tcg ggg gaa acc agc agc ggt ctt gat gca   713
Val Lys Arg Ser Thr Ser Ser Gly Glu Thr Ser Ser Gly Leu Asp Ala
155             160             165             170

gat ggc cac ttt aag cct tca ccc cag cca agg agc atg tta aaa aag   761
Asp Gly His Phe Lys Pro Ser Pro Gln Pro Arg Ser Met Leu Lys Lys
             175             180             185

agc agc cac act gag gag gga gtc aga cca gga gtt gat aaa gaa cat   809
Ser Ser His Thr Glu Glu Gly Val Arg Pro Gly Val Asp Lys Glu His
             190             195             200

tcc ata agc gaa gcc tct gct ccc aca cct tcc ctt cca agg cag aat   857
Ser Ile Ser Glu Ala Ser Ala Pro Thr Pro Ser Leu Pro Arg Gln Asn
             205             210             215

ggc aca gag ttg caa act gag gaa aaa ata tac tcg gaa aac ctc gat   905
Gly Thr Glu Leu Gln Thr Glu Glu Lys Ile Tyr Ser Glu Asn Leu Asp
             220             225             230

ctt gag gac tca ctc tta caa agt ctg acc tca tct tcc ttc aaa gaa   953
Leu Glu Asp Ser Leu Leu Gln Ser Leu Thr Ser Ser Phe Lys Glu
235             240             245             250

agc ccc gga ggt tgc aca tca cca gga tct cag gaa aag gtg ccc ata  1001
Ser Pro Gly Gly Cys Thr Ser Pro Gly Ser Gln Glu Lys Val Pro Ile
             255             260             265

aaa gat cat gat gga gaa cct act gaa atc tgg gat tcc ttg cta tca  1049
Lys Asp His Asp Gly Glu Pro Thr Glu Ile Trp Asp Ser Leu Leu Ser
             270             275             280

aat gaa aat gaa gga agt tct gtt ttg gtg aac tgt gtt act cct gaa  1097
Asn Glu Asn Glu Gly Ser Ser Val Leu Val Asn Cys Val Thr Pro Glu
             285             290             295

ctc gag cag ccc aag gac ggt cag gtg gca gct gac gac ctt gag gaa  1145
Leu Glu Gln Pro Lys Asp Gly Gln Val Ala Ala Asp Asp Leu Glu Glu
             300             305             310
```

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gaa aga gag aag ggt gga ttt aca gaa gat gac ctc acc act gac ccg    1193
Glu Arg Glu Lys Gly Gly Phe Thr Glu Asp Asp Leu Thr Thr Asp Pro
315             320             325             330

ctg ctc tcc acg tcc ccg agt gtc ata aca ccc act gag cca gca gag    1241
Leu Leu Ser Thr Ser Pro Ser Val Ile Thr Pro Thr Glu Pro Ala Glu
                335             340             345

ccg gcc aag aaa gca aat gaa gac aga aac acg aag aat aaa aag aca    1289
Pro Ala Lys Lys Ala Asn Glu Asp Arg Asn Thr Lys Asn Lys Lys Thr
            350             355             360

acg aat aac aga gtg tcc agt gcc tct ggc agc agg ctg atg acc tct    1337
Thr Asn Asn Arg Val Ser Ser Ala Ser Gly Ser Arg Leu Met Thr Ser
            365             370             375

gag ttt tta aag aga tcc ggt ccc aca aaa aga agt cca tct gca gct    1385
Glu Phe Leu Lys Arg Ser Gly Pro Thr Lys Arg Ser Pro Ser Ala Ala
    380             385             390

acc tcc tca cac tat tta ggg agt ttg aaa gtc ttg gac cag aag caa    1433
Thr Ser Ser His Tyr Leu Gly Ser Leu Lys Val Leu Asp Gln Lys Gln
395             400             405             410

cca cgg aag cag agc cta gag cca gac aag gct gat cac ata agg gca    1481
Pro Arg Lys Gln Ser Leu Glu Pro Asp Lys Ala Asp His Ile Arg Ala
            415             420             425

gct gtt tat cag gag tgg tta gaa aag aaa aat gtg tat tta cat gaa    1529
Ala Val Tyr Gln Glu Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu
            430             435             440

atg cac aga ata aaa aga att gaa agc gaa aac ttg agg atc caa aat    1577
Met His Arg Ile Lys Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn
            445             450             455

gaa cag aaa aaa gct gct aag aga gag gaa gcc ctg gca tca ttt gag    1625
Glu Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu
            460             465             470

gcc tgg aag gca atg aaa gag aag gaa gca aag aga ata gct gca aaa    1673
Ala Trp Lys Ala Met Lys Glu Lys Glu Ala Lys Arg Ile Ala Ala Lys
475             480             485             490

aag agg ctg gag gaa aag aac aag aag aaa aca gaa gaa gaa aat gcc    1721
Lys Arg Leu Glu Glu Lys Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala
            495             500             505

atg agg aaa ggc gag gcc ctg caa gca ttt gaa aaa tgg aaa gag aaa    1769
Met Arg Lys Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys
            510             515             520

aag cta gaa tac ctc aaa gag aag acc agg agg gag aaa gaa tat gaa    1817
Lys Leu Glu Tyr Leu Lys Glu Lys Thr Arg Arg Glu Lys Glu Tyr Glu
            525             530             535
```

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aga gca aag aaa cag aaa gaa gag gaa gcg gtt gct gag aaa aag aaa    1865
Arg Ala Lys Lys Gln Lys Glu Glu Glu Ala Val Ala Glu Lys Lys Lys
    540             545             550

gac agt tta act gct ttt gaa aaa tgg agt gag aga aag gaa gct ctc    1913
Asp Ser Leu Thr Ala Phe Glu Lys Trp Ser Glu Arg Lys Glu Ala Leu
555             560             565                 570

ctc aag caa aag gag aag gag aaa ata aat gag aga aga aag gaa gag    1961
Leu Lys Gln Lys Glu Lys Glu Lys Ile Asn Glu Arg Arg Lys Glu Glu
            575             580             585

ctg aag aga gcc gag aag aaa gac aaa gac aag caa gcc atc agt gaa    2009
Leu Lys Arg Ala Glu Lys Lys Asp Lys Asp Lys Gln Ala Ile Ser Glu
        590             595             600

tac gaa aag tgg ctg gaa aag aaa gaa agg caa gaa aga att gaa cgg    2057
Tyr Glu Lys Trp Leu Glu Lys Lys Glu Arg Gln Glu Arg Ile Glu Arg
        605             610             615

aaa cag aag aag cgc cac tcc ttc ctt gag agc gag aca cac cca cca    2105
Lys Gln Lys Lys Arg His Ser Phe Leu Glu Ser Glu Thr His Pro Pro
    620             625             630

tgg agt cct ccg agc aga act gcg ccc tca aaa gta ttt tga           2147
Trp Ser Pro Pro Ser Arg Thr Ala Pro Ser Lys Val Phe
635             640             645
```

```
tgtttctggt tcttgatttt tttttcagtt caccaactgt actcatggat ttaaaacgag 2207

tcatctcatt atttgtggtt agaagactct atgtcacttc cctgcaggag cttctgtgga 2267

gcatgaaaga gatactttgc agtttaatca gtggaaacat tttctgaagt gtcctcatca 2327

gtttgctggg acaatccaga cgcatgaagc tttattatga cctgaacagt ctggtgtggg 2387

gtgattcgtg gtcactgtcg ctgagttcgg agtctttta aagaatgttt gatcccacta 2447

atgaaagaat gccagctaga taccacaatc gtagagatga ctcggtctgt ggaagtctgt 2507

gcttctagag tgtagtttgg gcattgaagg tccctggaga ccatgggcat gttatctctt 2567

ctaactccag ttcttcaggt cacagaagta tctttgctgt gcaagttatc gactcagtca 2627

gttgaggcca cagaactcta gtcagtcact ttagtaaaga actttgccat agggtttaat 2687

ctcggtgtgg tttgccttct tgaggcttac ctgacaatcg tagccacctc tataatgggc 2747

tcacttctgg aatgttcttt                                             2767
```

<210> 46
<211> 647
<212> PRT
<213> Mus musculus

<400> 46

```
Met Ser Asp Glu Ile Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
 1               5                  10                  15

Lys Ala Thr Lys Arg Thr Ser Phe Gln Asp Glu Leu Ile Arg Ala Ile
            20                  25                  30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
        35                  40                  45

Asp Ser Asp Glu Ile Val Ser Leu Gly Glu Phe Ser Asp Thr Ser Thr
    50                  55                  60

Asp Glu Ser Leu Val Arg Lys Lys Met Asn Asp Phe His Ile Ser Asp
65                  70                  75                  80

Asp Glu Glu Lys Asn Ser Pro Arg Leu Ser Phe Leu Lys Thr Lys Lys
                85                  90                  95

Val Asn Arg Ala Ile Ser Asn Asp Ala Leu Asp Ser Ser Thr Pro Gly
            100                 105                 110

Ser Glu Gly Ser Ser Pro Asp Ala Gln Glu Asp Val Thr Gly Asp Ser
        115                 120                 125

Leu Pro Lys Ser Gln Asn Asp Asp Arg Glu Val Gly Arg Glu Ile Ile
    130                 135                 140

Thr Val Lys Pro Thr Pro Arg Met His Pro Val Lys Arg Ser Thr Ser
145                 150                 155                 160

Ser Gly Glu Thr Ser Ser Gly Leu Asp Ala Asp Gly His Phe Lys Pro
            165                 170                 175

Ser Pro Gln Pro Arg Ser Met Leu Lys Lys Ser Ser His Thr Glu Glu
        180                 185                 190

Gly Val Arg Pro Gly Val Asp Lys Glu His Ser Ile Ser Glu Ala Ser
        195                 200                 205

Ala Pro Thr Pro Ser Leu Pro Arg Gln Asn Gly Thr Glu Leu Gln Thr
    210                 215                 220

Glu Glu Lys Ile Tyr Ser Glu Asn Leu Asp Leu Glu Asp Ser Leu Leu
225                 230                 235                 240

Gln Ser Leu Thr Ser Ser Ser Phe Lys Glu Ser Pro Gly Gly Cys Thr
            245                 250                 255

Ser Pro Gly Ser Gln Glu Lys Val Pro Ile Lys Asp His Asp Gly Glu
        260                 265                 270

Pro Thr Glu Ile Trp Asp Ser Leu Leu Ser Asn Glu Asn Glu Gly Ser
    275                 280                 285

Ser Val Leu Val Asn Cys Val Thr Pro Glu Leu Glu Gln Pro Lys Asp
    290                 295                 300
```

Gly Gln Val Ala Ala Asp Asp Leu Glu Glu Glu Arg Glu Lys Gly Gly
305   310   315   320

Phe Thr Glu Asp Asp Leu Thr Thr Asp Pro Leu Leu Ser Thr Ser Pro
                325   330   335

Ser Val Ile Thr Pro Thr Glu Pro Ala Glu Pro Ala Lys Lys Ala Asn
                340   345   350

Glu Asp Arg Asn Thr Lys Asn Lys Lys Thr Thr Asn Asn Arg Val Ser
            355   360   365

Ser Ala Ser Gly Ser Arg Leu Met Thr Ser Glu Phe Leu Lys Arg Ser
        370   375   380

Gly Pro Thr Lys Arg Ser Pro Ser Ala Ala Thr Ser Ser His Tyr Leu
385   390   395   400

Gly Ser Leu Lys Val Leu Asp Gln Lys Gln Pro Arg Lys Gln Ser Leu
                405   410   415

Glu Pro Asp Lys Ala Asp His Ile Arg Ala Ala Val Tyr Gln Glu Trp
            420   425   430

Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys Arg
            435   440   445

Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala Ala
        450   455   460

Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys Ala Met Lys
465   470   475   480

Glu Lys Glu Ala Lys Arg Ile Ala Ala Lys Lys Arg Leu Glu Glu Lys
                485   490   495

Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala Met Arg Lys Gly Glu Ala
                500   505   510

Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Leu Glu Tyr Leu Lys
            515   520   525

Glu Lys Thr Arg Arg Glu Lys Glu Tyr Glu Arg Ala Lys Lys Gln Lys
        530   535   540

Glu Glu Glu Ala Val Ala Glu Lys Lys Lys Asp Ser Leu Thr Ala Phe
545   550   555   560

Glu Lys Trp Ser Glu Arg Lys Glu Ala Leu Leu Lys Gln Lys Glu Lys
                565   570   575

Glu Lys Ile Asn Glu Arg Arg Lys Glu Glu Leu Lys Arg Ala Glu Lys
            580   585   590

Lys Asp Lys Asp Lys Gln Ala Ile Ser Glu Tyr Glu Lys Trp Leu Glu
        595   600   605

Lys Lys Glu Arg Gln Glu Arg Ile Glu Arg Lys Gln Lys Lys Arg His
    610   615   620

Ser Phe Leu Glu Ser Glu Thr His Pro Pro Trp Ser Pro Pro Ser Arg
625   630   635   640

Thr Ala Pro Ser Lys Val Phe
                645

<210> 47
<211> 647
<212> PRT
<213> Mus musculus

<400> 47
Met Ser Asp Glu Ile Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
  1   5   10   15

Lys Ala Thr Lys Arg Thr Ser Phe Gln Asp Glu Leu Ile Arg Ala Ile
            20   25   30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
          35   40   45

Asp Ser Asp Glu Ile Val Ser Leu Gly Glu Phe Ser Asp Thr Ser Thr
      50   55   60

Asp Glu Ser Leu Val Arg Lys Lys Met Asn Asp Phe His Ile Ser Asp
65   70   75   80

Asp Glu Glu Lys Asn Ser Pro Arg Leu Ser Phe Leu Lys Thr Lys Lys
              85   90   95

Val Asn Arg Ala Ile Ser Asn Asp Ala Leu Asp Ser Ser Thr Pro Gly
            100   105   110

Ser Glu Gly Ser Ser Pro Asp Ala Gln Glu Asp Val Thr Gly Asp Ser
          115   120   125

Leu Pro Lys Ser Gln Asn Asp Asp Arg Glu Val Gly Arg Glu Ile Ile
    130   135   140

Thr Val Lys Pro Thr Pro Arg Met His Pro Val Lys Arg Ser Thr Ser
145   150   155   160

Ser Gly Glu Thr Ser Ser Gly Leu Asp Ala Asp Gly His Phe Lys Pro
                165   170   175

Ser Pro Gln Pro Arg Ser Met Leu Lys Lys Ser Ser His Thr Glu Glu
            180   185   190

Gly Val Arg Pro Gly Val Asp Lys Glu His Ser Ile Ser Glu Ala Ser
          195   200   205

Ala Pro Thr Pro Ser Leu Pro Arg Gln Asn Gly Thr Glu Leu Gln Thr
    210   215   220

Glu Glu Lys Ile Tyr Ser Glu Asn Leu Asp Leu Glu Asp Ser Leu Leu
225   230   235   240

Gln Ser Leu Thr Ser Ser Ser Phe Lys Glu Ser Pro Gly Gly Cys Thr
                245   250   255

Ser Pro Gly Ser Gln Glu Lys Val Pro Ile Lys Asp His Asp Gly Glu
            260   265   270

Pro Thr Glu Ile Trp Asp Ser Leu Leu Ser Asn Glu Asn Glu Gly Ser
        275   280   285

Ser Val Leu Val Asn Cys Val Thr Pro Glu Leu Glu Gln Pro Lys Asp
        290   295   300

Gly Gln Val Ala Ala Asp Asp Leu Glu Glu Glu Arg Glu Lys Gly Gly
305   310   315   320

Phe Thr Glu Asp Asp Leu Thr Thr Asp Pro Leu Leu Ser Thr Ser Pro
                325   330   335

Ser Val Ile Thr Pro Thr Glu Pro Ala Glu Pro Ala Lys Lys Ala Asn
            340   345   350

Glu Asp Arg Asn Thr Lys Asn Lys Lys Thr Thr Asn Asn Arg Val Ser
        355   360   365

Ser Ala Ser Gly Ser Arg Leu Met Thr Ser Glu Phe Leu Lys Arg Ser
        370   375   380

Gly Pro Thr Lys Arg Ser Pro Ser Ala Ala Thr Ser Ser His Tyr Leu
385   390   395   400

Gly Ser Leu Lys Val Leu Asp Gln Lys Gln Pro Arg Lys Gln Ser Leu
                405   410   415

Glu Pro Asp Lys Ala Asp His Ile Arg Ala Ala Val Tyr Gln Glu Trp
            420   425   430

Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys Arg
        435   440   445

Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala Ala
        450   455   460

Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys Ala Met Lys
465   470   475   480

Glu Lys Glu Ala Lys Arg Ile Ala Ala Lys Lys Arg Leu Glu Glu Lys
                485   490   495

Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala Met Arg Lys Gly Glu Ala
            500   505   510

Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Leu Glu Tyr Leu Lys
        515   520   525

```
Glu Lys Thr Arg Arg Glu Lys Glu Tyr Glu Arg Ala Lys Lys Gln Lys
    530             535             540

Glu Glu Glu Ala Val Ala Glu Lys Lys Lys Asp Ser Leu Thr Ala Phe
545             550             555             560

Glu Lys Trp Ser Glu Arg Lys Glu Ala Leu Leu Lys Gln Lys Glu Lys
            565             570             575

Glu Lys Ile Asn Glu Arg Arg Lys Glu Glu Leu Lys Arg Ala Glu Lys
            580             585             590

Lys Asp Lys Asp Lys Gln Ala Ile Ser Glu Tyr Glu Lys Trp Leu Glu
        595             600             605

Lys Lys Glu Arg Gln Glu Arg Ile Glu Arg Lys Gln Lys Lys Arg His
    610             615             620

Ser Phe Leu Glu Ser Glu Thr His Pro Pro Trp Ser Pro Pro Ser Arg
625             630             635             640

Thr Ala Pro Ser Lys Val Phe
                645
```

<210> 48
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

<400> 48
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Glu Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Glu Lys Ala Lys Ala
 1              5               10              15

Glu Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys
            20              25              30

Ser Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys
        35              40              45

Thr Ile Glu Asp Arg Asn Ile Lys Asn Lys Lys Ser Thr Asn Asn Arg
    50              55              60

Ala Ser Ser Ala Ser Ala Arg Leu Met Thr Ser Glu Phe Leu Lys Lys
65              70              75              80

Ser Ser Ser Lys Arg Arg Thr Pro Ser Thr Thr Thr Ser Ser His Tyr
            85              90              95

Leu Gly Thr Leu Lys Val Leu Asp Gln Lys Pro Ser Gln Lys Gln Ser
            100             105             110

Ile Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala Ala Val Tyr Gln Glu
        115             120             125
```

Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys
   130   135   140

Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala
145   150   155   160

Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys Ala Met
          165   170   175

Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys Lys Arg Leu Glu Glu
          180   185   190

Lys Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala Ala Arg Lys Gly Glu
          195   200   205

Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Met Glu Tyr Leu
          210   215   220

Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu Arg Ala Lys Lys Gln
225   230   235   240

Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys Asp Asn Leu Thr Ala
          245   250   255

Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe Phe Lys Gln Lys Lys
          260   265   270

Lys Glu Lys Ile Asn Glu Lys Arg Lys Glu Glu Leu Lys Arg Ala Glu
          275   280   285

Lys Lys Asp Lys Asp Lys Gln Ala Ile Asn Glu Tyr Glu Lys Trp Leu
          290   295   300

Glu Asn Lys Glu Lys Gln Glu Arg Ile Glu Arg Lys Gln Lys Lys Arg
305   310   315   320

His Ser Phe Leu Glu Ser Glu Ala Leu Pro Pro Trp Ser Pro Pro Ser
          325   330   335

Arg Thr Val Phe Ala Lys Val Phe
          340

<210> 49
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     protein sequence

<400> 49
Ser Gln Lys Gln Ser Ile Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala
  1   5   10   15

Ala Val Tyr Gln Glu Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu
            20   25   30

Met His Arg Ile Lys Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn
            35   40   45

Glu Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu
        50   55   60

Ala Trp Lys Ala Met Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys
65   70   75   80

Lys Arg Leu Glu Glu Lys Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala
                    85   90   95

Ala Arg Lys Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys
            100   105   110

Lys Met Glu Tyr Leu Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu
            115   120   125

Arg Ala Lys Lys Gln Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys
    130   135   140

Asp Asn Leu Thr Ala Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe
145   150   155   160

Phe Lys Gln Lys Lys Lys Glu Lys Ile Asn Glu Lys Arg Lys Glu Glu
                165   170   175

Leu Lys Arg Ala Glu Lys Lys Asp Lys Asp Lys Gln Ala Ile Asn Glu
            180   185   190

Tyr Glu Lys Trp Leu Glu Asn Lys Glu Lys Gln Glu Arg Ile Glu Arg
            195   200   205

Lys Gln Lys Lys Arg His Ser Phe Leu Glu Ser Glu Ala Leu Pro Pro
    210   215   220

Trp Ser Pro Pro Ser Arg Thr Val Phe Ala Lys Val Phe
225   230   235

<210> 50
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

<400> 50
Ala Met Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys Lys Arg Leu
    1   5   10   15

Glu Glu Lys Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala Ala Arg Lys
            20   25   30

Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Met Glu
        35   40   45

Tyr Leu Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu Arg Ala Lys
    50   55   60

Lys Gln Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys Asp Asn Leu
65   70   75   80

Thr Ala Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe Phe Lys Gln
                85   90   95

Lys Lys Lys Glu Lys Ile Asn Glu Lys Arg Lys Glu Glu Leu Lys Arg
            100   105   110

Ala Glu Lys Lys Asp Lys Asp Lys Gln Ala Ile Asn Glu Tyr Glu Lys
        115   120   125

Trp Leu Glu Asn Lys Glu Lys Gln Glu Arg Ile Glu Arg Lys Gln Lys
    130   135   140

Lys Arg His Ser Phe Leu Glu Ser Glu Ala Leu Pro Pro Trp Ser Pro
145   150   155   160

Pro Ser Arg Thr Val Phe Ala Lys Val Phe
                165   170

<210> 51
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

<400> 51
Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
  1   5   10   15

Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
            20   25   30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
        35   40   45

Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
    50   55   60

Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
65   70   75   80

Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
                85   90   95

Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
        100   105   110

Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
        115   120   125

Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
    130   135   140

Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
145   150   155   160

Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
            165   170   175

Trp Pro Arg Ser Met Leu Lys Lys Lys Ser His Met Glu Glu Lys Asp
            180   185   190

Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
        195   200   205

Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
    210   215   220

Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
225   230   235   240

Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
            245   250   255

Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
            260   265   270

Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
        275   280   285

Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys Glu
    290   295   300

Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Glu Lys Ala Lys Ala Glu
305   310   315   320

Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys Ser
            325   330   335

Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys Thr
            340   345   350

Ile Glu Asp Arg Asn Ile Lys Asn Lys Lys Ser Thr Asn Asn Arg Ala
        355   360   365

Ser Ser Ala Ser Ala Arg Leu Met Thr Ser Glu Phe Leu Lys Lys Ser
    370   375   380

Ser Ser Lys Arg Arg Thr Pro Ser Thr Thr Thr Ser Ser His Tyr Leu
385   390   395   400

Gly Thr Leu Lys Val Leu Asp Gln Lys Pro Ser Gln Lys Gln Ser Ile
                405   410   415

Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala Ala Val Tyr Gln Glu Trp
            420   425   430

Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys Arg
        435   440   445

Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala Ala
    450   455   460

Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys
465   470   475

<210> 52
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

<400> 52
Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
  1   5   10   15

Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
            20   25   30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
        35   40   45

Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
    50   55   60

Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
65   70   75   80

Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
            85   90   95

Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
            100   105   110

Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
        115   120   125

Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
    130   135   140

Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
145   150   155   160

Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
            165   170   175

Trp Pro Arg Ser Met Leu Lys Lys Lys Ser His Met Glu Glu Lys Asp
            180   185   190

Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
        195   200   205

Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
        210   215   220

Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
225   230   235   240

Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
            245   250   255

Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
            260   265   270

Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
        275   280   285

Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys Glu
        290   295   300

Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Glu Lys Ala Lys Ala Glu
305   310   315   320

Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys Ser
            325   330   335

Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys Thr
            340   345   350

Ile Glu Asp Arg Asn Ile Lys Asn Lys Lys Ser Thr Asn Asn Arg Ala
        355   360   365

Ser Ser Ala Ser Ala Arg Leu Met Thr Ser Glu Phe Leu Lys Lys Ser
        370   375   380

Ser Ser Lys Arg Arg Thr Pro Ser Thr Thr Thr Ser Ser His Tyr Leu
385   390   395   400

Gly Thr Leu Lys Val Leu Asp Gln Lys Pro Ser Gln Lys Gln Ser Ile
            405   410   415

Glu Pro

<210> 53
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      protein sequence

<400> 53

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Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
 1               5                  10                  15

Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
            20                  25                  30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
        35                  40                  45

Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
    50                  55                  60

Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
65                  70                  75                  80

Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
                85                  90                  95

Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
            100                 105                 110

Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
        115                 120                 125

Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
    130                 135                 140

Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
145                 150                 155                 160

Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
                165                 170                 175

Trp Pro Arg Ser Met Leu Lys Lys Lys Ser His Met Glu Glu Lys Asp
            180                 185                 190

Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
        195                 200                 205

Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
    210                 215                 220

Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
225                 230                 235                 240

Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
                245                 250                 255

Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
            260                 265                 270

Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
        275                 280                 285

Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys
    290                 295                 300
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